

SEQUENCE LISTING

<110> Wakamiya, N.

<120> Novel Collectin

<130> 19036/37157

<150> JP HEI 10-237611

<151> 1998-08-24

<160> 32

<210> 1

<211> 2024

<212> DNA

<213> Homo Sapiens

<220>

<221> CDS

<222> (670)..(1695)

<400> 1

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aacctcatca cgaatctgca gcggctgtg gatgacacaa gccaggctat ccagcgaatc	180
aagaacgact ttcaaaatct gcagcagggtt ttcttcagg ccaagaagga cacggattgg	240
ctgaaggaga aagtgcagag cttgcagacg ctggctgcca acaactctgc gttggccaaa	300
gccaacaacg acaccctgga ggatatgaac agccagctca actcattcac aggtcagatg	360
gagaacatca ccactatctc tcaagccaaac gagcagaacc tgaaagacct gcaggactta	420
cacaagatg cagagaatag aacagccatc aagttcaacc aactggagga acgcttccag	480
ctctttgaga cggatattgt gaacatcatt agcaatatca gttacacagc ccaccacctg	540
cggacgctga ccagcaatct aaatgaagtc aggaccactt gcacagatac ctttacccaa	600
cacacagatg atctgaccc tttgataat accctggcca acatccgtt ggattctgtt	660
tctctcagg atg caa gat ttg atg agg tcg agg tta gac act gaa gta	711
Met Gln Gln Asp Leu Met Arg Ser Arg Leu Asp Thr Glu Val	
1 5 10	
gcc aac tta tca gtg att atg gaa gaa atg aag cta gta gac tcc aag	759
Ala Asn Leu Ser Val Ile Met Glu Glu Met Lys Leu Val Asp Ser Lys	
15 20 25 30	
cat ggt cag ctc atc aag aat ttt aca ata cta caa ggt cca ccg ggc	807
His Gly Gln Leu Ile Lys Asn Phe Thr Ile Leu Gln Gly Pro Pro Gly	
35 40 45	
ccc agg ggt cca aga ggt gac aga gga tcc cag gga ccc cct ggc cca	855
Pro Arg Gly Pro Arg Gly Asp Arg Gly Ser Gln Gly Pro Pro Gly Pro	
50 55 60	
act ggc aac aag gga cag aaa gga gag aag ggg gag cct gga cca cct	903
Thr Gly Asn Lys Gly Gln Lys Gly Glu Lys Gly Glu Pro Gly Pro Pro	
65 70 75	
ggc cct gcg ggt gag aga ggc cca att gga cca gct ggt ccc ccc gga	951
Gly Pro Ala Gly Glu Arg Gly Pro Ile Gly Pro Ala Gly Pro Pro Gly	
80 85 90	
gag cgt ggc ggc aaa gga tct aaa ggc tcc cag ggc ccc aaa ggc tcc	999
Glu Arg Gly Lys Gly Ser Lys Gly Ser Gln Gly Pro Lys Gly Ser	
95 100 105 110	
cgt ggt tcc cct ggg aag ccc ggc cct cag ggc ccc agt ggg gac cca	1047
Arg Gly Ser Pro Gly Lys Pro Gly Pro Gln Gly Pro Ser Gly Asp Pro	
115 120 125	
ggc ccc ccc ggc cca gca ggc aaa gag gga ctc ccc ggc cct cag ggc	1095
Gly Pro Pro Gly Pro Pro Gly Lys Glu Gly Leu Pro Gly Pro Gln Gly	
130 135 140	

cct cct ggc ttc cag gga ctt cag ggc acc gtt ggg gag cct ggg gtg	1143
Pro Pro Gly Phe Gln Gly Leu Gln Gly Thr Val Gly Glu Pro Gly Val	
145 150 155	
cct gga cct cgg gga ctg cca ggc ttg cct ggg gta cca ggc atg cca	1191
Pro Gly Pro Arg Gly Leu Pro Gly Leu Pro Gly Val Pro Gly Met Pro	
160 165 170	
ggc ccc aag ggc ccc ccc ggc cct cct ggc cca tca gga gcg gtg gtg	1239
Gly Pro Lys Gly Pro Pro Gly Pro Pro Gly Pro Ser Gly Ala Val Val	
175 180 185 190	
ccc ctg gcc ctg cag aat gag cca acc ccg gca ccg gag gac aat ggc	1287
Pro Leu Ala Leu Gln Asn Glu Pro Thr Pro Ala Pro Glu Asp Asn Gly	
195 200 205	
tgc ccg cct cac tgg aag aac ttc aca gac aaa tgc tac tat ttt tca	1335
Cys Pro Pro His Trp Lys Asn Phe Thr Asp Lys Cys Tyr Tyr Phe Ser	
210 215 220	
gtt gag aaa gaa att ttt gag gat gca aag ctt ttc tgt gaa gac aag	1383
Val Glu Lys Glu Ile Phe Glu Asp Ala Lys Leu Phe Cys Glu Asp Lys	
225 230 235	
tct tca cat ctt gtt ttc ata aac act aga gag gaa cag caa tgg ata	1431
Ser Ser His Leu Val Phe Ile Asn Thr Arg Glu Glu Gln Gln Trp Ile	
240 245 250	
aaa aaa cag atg gta ggg aga gag agc cac tgg atc ggc ctc aca gac	1479
Lys Lys Gln Met Val Gly Arg Glu Ser His Trp Ile Gly Leu Thr Asp	
255 260 265 270	
tca gag cgt gaa aat gaa tgg aag tgg ctg gat ggg aca tct cca gac	1527
Ser Glu Arg Glu Asn Glu Trp Lys Trp Leu Asp Gly Thr Ser Pro Asp	
275 280 285	
tac aaa aat tgg aaa gct gga cag ccg gat aac tgg ggt cat ggc cat	1575
Tyr Lys Asn Trp Lys Ala Gly Gln Pro Asp Asn Trp Gly His Gly His	
290 295 300	
ggg cca gga gaa gac tgt gct ggg ttg att tat gct ggg cag tgg aac	1623
Gly Pro Gly Glu Asp Cys Ala Gly Leu Ile Tyr Ala Gly Gln Trp Asn	
305 310 315	
gat ttc caa tgt gaa gac gtc aat aac ttc att tgc gaa aaa gac agg	1671
Asp Phe Gln Cys Glu Asp Val Asn Asn Phe Ile Cys Glu Lys Asp Arg	
320 325 330	
gag aca gta ctg tca tct gca tta taacggactg tgatggatc acatgagcaa	1725
Glu Thr Val Leu Ser Ser Ala Leu	
335 340	
attttcagct ctcaaaggca aaggacactc ctttctaatt gcatcacctt ctcatacgat	1785
tgaaaaaaaaaaa aaaagcactg aaaaccaatt actgaaaaaaaaa aattgacagc tagtgttttt	1845
taccatccgt cattacccaa agacttggga actaaaaatgt tccccagggat gatatgctga	1905
ttttcattgt gcacatggac tgaatcacat agattctcct ccgtcagtaa ccgtgcgatt	1965
atacaaatta tgtcttccaa agtatggaac actccaatca gaaaaaggtt atcatcccg	2024

<210> 2

<211> 547

<212> PRT

<213> Homo Sapiens

<220>

<223> Dduced Amino Acid Sequence of Novel Collectin from Nucleotide Sequence

<400>2

Met Tyr Ser His Asn Val Val Ile Met Asn Leu Asn Asn Leu Asn Leu	
1 5 10 15	
Thr Gln Val Gln Gln Arg Asn Leu Ile Thr Asn Leu Gln Arg Ser Val	
20 25 30	
Asp Asp Thr Ser Gln Ala Ile Gln Arg Ile Lys Asn Asp Phe Gln Asn	
35 40 45	
Leu Gln Gln Val Phe Leu Gln Ala Lys Lys Asp Thr Asp Trp Leu Lys	
50 55 60	

Glu Lys Val Gln Ser Leu Gln Thr Leu Ala Ala Asn Asn Ser Ala Leu
 65 70 75 80
 Ala Lys Ala Asn Asn Asp Thr Leu Glu Asp Met Asn Ser Gln Leu Asn
 85 90 95
 Ser Phe Thr Gly Gln Met Glu Asn Ile Thr Thr Ile Ser Gln Ala Asn
 100 105 110
 Glu Gln Asn Leu Lys Asp Leu Gln Asp Leu His Lys Asp Ala Glu Asn
 115 120 125
 Arg Thr Ala Ile Lys Phe Asn Gln Leu Glu Glu Arg Phe Gln Leu Phe
 130 135 140
 Glu Thr Asp Ile Val Asn Ile Ile Ser Asn Ile Ser Tyr Thr Ala His
 145 150 155 160
 His Leu Arg Thr Leu Thr Ser Asn Leu Asn Glu Val Arg Thr Thr Cys
 165 170 175
 Thr Asp Thr Leu Thr Lys His Thr Asp Asp Leu Thr Ser Leu Asn Asn
 180 185 190
 Thr Leu Ala Asn Ile Arg Leu Asp Ser Val Ser Leu Arg Met Gln Gln
 195 200 205
 Asp Leu Met Arg Ser Arg Leu Asp Thr Glu Val Ala Asn Leu Ser Val
 210 215 220
 Ile Met Glu Glu Met Lys Leu Val Asp Ser Lys His Gly Gln Leu Ile
 225 230 235 240
 Lys Asn Phe Thr Ile Leu Gln Gly Pro Pro Gly Pro Arg Gly Pro Arg
 245 250 255
 Gly Asp Arg Gly Ser Gln Gly Pro Pro Gly Pro Thr Gly Asn Lys Gly
 260 265 270
 Gln Lys Gly Glu Lys Gly Glu Pro Gly Pro Pro Gly Pro Ala Gly Glu
 275 280 285
 Arg Gly Pro Ile Gly Pro Ala Gly Pro Pro Gly Glu Arg Gly Gly Lys
 290 295 300
 Gly Ser Lys Gly Ser Gln Gly Pro Lys Gly Ser Arg Gly Ser Pro Gly
 305 310 315 320
 Lys Pro Gly Pro Gln Gly Pro Ser Gly Asp Pro Gly Pro Pro Gly Pro
 325 330 335
 Pro Gly Lys Glu Gly Leu Pro Gly Pro Gln Gly Pro Pro Gly Phe Gln
 340 345 350
 Gly Leu Gln Gly Thr Val Gly Glu Pro Gly Val Pro Gly Pro Arg Gly
 355 360 365
 Leu Pro Gly Leu Pro Gly Val Pro Gly Met Pro Gly Pro Lys Gly Pro
 370 375 380
 Pro Gly Pro Pro Gly Pro Ser Gly Ala Val Val Pro Leu Ala Leu Gln
 385 390 395 400
 Asn Glu Pro Thr Pro Ala Pro Glu Asp Asn Gly Cys Pro Pro His Trp
 405 410 415
 Lys Asn Phe Thr Asp Lys Cys Tyr Tyr Phe Ser Val Glu Lys Glu Ile
 420 425 430
 Phe Glu Asp Ala Lys Leu Phe Cys Glu Asp Lys Ser Ser His Leu Val
 435 440 445
 Phe Ile Asn Thr Arg Glu Glu Gln Gln Trp Ile Lys Lys Gln Met Val
 450 455 460
 Gly Arg Glu Ser His Trp Ile Gly Leu Thr Asp Ser Glu Arg Glu Asn
 465 470 475 480
 Glu Trp Lys Trp Leu Asp Gly Thr Ser Pro Asp Tyr Lys Asn Trp Lys
 485 490 495
 Ala Gly Gln Pro Asp Asn Trp Gly His Gly His Gly Pro Gly Glu Asp
 500 505 510
 Cys Ala Gly Leu Ile Tyr Ala Gly Gln Trp Asn Asp Phe Gln Cys Glu
 515 520 525
 Asp Val Asn Asn Phe Ile Cys Glu Lys Asp Arg Glu Thr Val Leu Ser
 530 535 540
 Ser Ala Leu
 545

<210> 3
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified Consensus Sequence of collectins Hybridizable with Novel Collectin

<400>3
Glu Lys Cys Val Glu Met Tyr Thr Asp Gly Lys Trp Asn Asp Arg Asn
1 5 10 15
Cys Leu Gln Ser Arg Leu Ala Ile Cys Glu Phe
20 25

<210> 4
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence of a Reverse Primer for Screening a Novel Collectin.

<400> 4
caatctgtatg agaagggtat g

21

<210> 5
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence of a Forward Primer for Screening a Novel Collectin.

<400> 5
acgaggggct ggatgggaca t

21

<210> 6
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence of three collectins which were reported heretofore

<400>6
Glu Asp Cys Val Leu Leu Leu Lys Asn Gly Gln Trp Asn Asp Val Pro
1 5 10 15
Cys Ser Thr Ser His Leu Ala Val Cys Glu Phe
20 25

<210> 7
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> M13 Universal Primer Sequence for Sequencing

<400> 7
cgacgttgta aaacgcacggc cagt

24

<210> 8
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> M13 Reverse Primer Sequence for Sequencing.

<400> 8
cagggaaaca gctatgac 17

<210> 9
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence of a lambda gt11 Reverse Primer for Sequencing.

<400> 9
ttgacaccag accaactgggt aatg 24

<210> 10
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence of a lambda gt11 Forward Primer for Sequencing.

<400> 10
ggtggcgacg actcctggag cccg 24

<210> 11
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence of a Primer for Screening a Novel Collectin

<400>11
cgtaaaaatg aatggaagtg g 21

<210> 12
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence of a Primer for Screening a Novel Collectin

<400>12
tttatccat tgctgttcct c 21

<210> 13
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence of a Primer for Sequencing a Novel Collectin

<400>13
ctggcagtcc ccgaggtcca g 21

<210> 14
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence of a Primer for Sequencing a Novel Collectin

<400>14
gctggtcccc ccggagagcg t 21

<210> 15
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence of a 1RC2 Primer for Cap Site Sequencing

<400> 15
caaggtacgc cacagcgtat g 21

<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence of a Synthetic TGP1 Primer for Cap Site Sequencing

<400> 16
tcttcagttt ccctaattccc 20

<210> 17
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence of a 2RC2 Primer for Cap Site Sequencing

<400> 17
gtacgccaca gcgttatgtat c 21

<210> 18
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence of a Synthetic TGP2 Primer for Cap Site Sequencing

<400> 18
cattcttgac aaacttcata g 21

<210> 19
<211> 22
<212> DNA
<213> Artificial Sequence

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<220>
<223> Sequence of a Primer for Screening a Novel Collectin

<400> 19
gaagacaagt cttcaactct tg 22

<210> 20
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence of a Primer for Screening a Novel Collectin

<400> 20
ctctgagtct gtgaggccga tc 22

<210> 21
<211> 111
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence of a Probe for Screening a Novel Collectin

<400> 21
gaagacaagt ctgcacatct tgggttcata aacactagag aggaacagca atggataaaa 60
aaacagatgg tagggagaga gagccactgg atcggcctca cagactcaga g 111

<210> 22
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence of a Forward Primer for Screening a Novel Collectin

<400> 22
gtgcccctgg ccctgcagaa tg 22

<210> 23
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence of a Reverse Primer for Screening a Novel Collectin

<400> 23
gcataatcacc ctggggaaaca ttttag 26

<210> 24
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence of a Sense Primer for Screening Beta Actin

<400> 24
caagagatgg ccacggctgc t 21

<210> 25

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<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence of an Antisense Primer for Screening Beta Actin

<400> 25
tccttctgca tcctgtcggt a 21

<210> 26
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence of a Sense Primer for Amplifying the Novel Collectin.

<400> 26
aaggaaaaaa gcggccgcatt gcaacaagat ttgatgagg 39

<210> 27
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence of a Reverse Primer for Amplifying the Novel Collectin

<400> 27
gctcttagatt ataatgcaga tgacagtac 29

<210> 28
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence of a Sense Primer for Amplifying the Nockout Gene

<400> 28
atgcaacaag atttgatgag g 21

<210> 29
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence of a Sense Primer for Amplifying the Nockout Gene

<400> 29
cctaccgggt agaattgacc 20

<210> 30
<211> 248
<212> PRT
<213> Homo sapiens

<220>
<223> mannan-binding protein (MBP)

<400> 30
Met Ser Leu Phe Pro Ser Leu Pro Leu Leu Leu Ser Met Val Ala
1 5 10 15

Ala Ser Tyr Ser Glu Thr Val Thr Cys Glu Asp Ala Gln Lys Thr Cys
20 25 30

Pro Ala Val Ile Ala Cys Ser Ser Pro Gly Ile Asn Gly Phe Pro Gly
35 40 45

Lys Asp Gly Arg Asp Gly Thr Lys Gly Glu Lys Gly Glu Pro Gly Gln
50 55 60

Gly Leu Arg Gly Leu Gln Gly Pro Pro Gly Lys Leu Gly Pro Pro Gly
65 70 75 80

Asn Pro Gly Pro Ser Gly Ser Pro Gly Pro Lys Gly Gln Lys Gly Asp
85 90 95

Pro Gly Lys Ser Pro Asp Gly Asp Ser Ser Leu Ala Ala Ser Glu Arg
100 105 110

Lys Ala Leu Gln Thr Glu Met Ala Arg Ile Lys Lys Trp Leu Thr Phe
115 120 125

Ser Leu Gly Lys Gln Val Gly Asn Lys Phe Phe Leu Thr Asn Gly Glu
130 135 140

Ile Met Thr Phe Glu Lys Val Lys Ala Leu Cys Val Lys Phe Gln Ala
145 150 155 160

Ser Val Ala Thr Pro Arg Asn Ala Ala Glu Asn Gly Ala Ile Gln Asn
165 170 175

Leu Ile Lys Glu Glu Ala Phe Leu Gly Ile Thr Asp Glu Lys Thr Glu
180 185 190

Gly Gln Phe Val Asp Leu Thr Gly Asn Arg Leu Thr Tyr Thr Asn Trp
195 200 205

Asn Glu Gly Glu Pro Asn Asn Ala Gly Ser Asp Glu Asp Cys Val Leu
210 215 220

Leu Leu Lys Asn Gly Gln Trp Asn Asp Val Pro Cys Ser Thr Ser His
225 230 235 240

Leu Ala Val Cys Glu Phe Pro Ile
245

<210> 31
<211> 248
<212> PRT
<213> Homo sapiens

<220>
<223> surfactant protein A (SP-A)

<400> 31
Met Trp Leu Cys Pro Leu Ala Leu Thr Leu Ile Leu Met Ala Ala Ser
1 5 10 15

Gly Ala Ala Cys Glu Val Lys Asp Val Cys Val Gly Ser Pro Gly Ile
 20 25 30

Pro Gly Thr Pro Gly Ser His Gly Leu Pro Gly Arg Asp Gly Arg Asp
 35 40 45

Gly Val Lys Gly Asp Pro Gly Pro Pro Gly Pro Met Gly Pro Pro Gly
 50 55 60

Glu Thr Pro Cys Pro Pro Gly Asn Asn Gly Leu Pro Gly Ala Pro Gly
 65 70 75 80

Val Pro Gly Glu Arg Gly Glu Lys Gly Glu Pro Gly Glu Arg Gly Pro
 85 90 95

Pro Gly Leu Pro Ala His Leu Asp Glu Glu Leu Gln Ala Thr Leu His
 100 105 110

Asp Phe Arg His Gln Ile Leu Gln Thr Arg Gly Ala Leu Ser Leu Gln
 115 120 125

Gly Ser Ile Met Thr Val Gly Glu Lys Val Phe Ser Ser Asn Gly Gln
 130 135 140

Ser Ile Thr Phe Asp Ala Ile Gln Glu Ala Cys Ala Arg Ala Gly Gly
 145 150 155 160

Arg Ile Ala Val Pro Arg Asn Pro Glu Glu Asn Glu Ala Ile Ala Ser
 165 170 175

Phe Val Lys Lys Tyr Asn Thr Tyr Ala Tyr Val Gly Leu Thr Glu Gly
 180 185 190

Pro Ser Pro Gly Asp Phe Arg Tyr Ser Asp Gly Thr Pro Val Asn Tyr
 195 200 205

Thr Asn Trp Tyr Arg Gly Glu Pro Ala Gly Arg Gly Lys Glu Gln Cys
 210 215 220

Val Glu Met Tyr Thr Asp Gly Gln Trp Asn Asp Arg Asn Cys Leu Tyr
 225 230 235 240

Ser Arg Leu Thr Ile Cys Glu Phe
 245

<210> 32
 <211> 375
 <212> PRT
 <213> Homo sapiens

<220>
 <223> surfactant protein D (SP-D)

<400> 32
 Met Leu Leu Phe Leu Leu Ser Ala Leu Val Leu Leu Thr Gln Pro Leu
 1 5 10 15

Gly Tyr Leu Glu Ala Glu Met Lys Thr Tyr Ser His Arg Thr Thr Pro
 20 25 30

Ser Ala Cys Thr Leu Val Met Cys Ser Ser Val Glu Ser Gly Leu Pro
 35 40 45

Gly Arg Asp Gly Arg Asp Gly Arg Glu Gly Pro Arg Gly Glu Lys Gly
 50 55 60

Asp Pro Gly Leu Pro Gly Ala Ala Gly Gln Ala Gly Met Pro Gly Gln
 65 70 75 80

Ala Gly Pro Val Gly Pro Lys Gly Asp Asn Gly Ser Val Gly Glu Pro
 85 90 95

Gly Pro Lys Gly Asp Thr Gly Pro Ser Gly Pro Pro Gly Pro Pro Gly
 100 105 110

Val Pro Gly Pro Ala Gly Arg Glu Gly Pro Leu Gly Lys Gln Gly Asn
 115 120 125

Ile Gly Pro Gln Gly Lys Pro Gly Pro Lys Gly Glu Ala Gly Pro Lys
 130 135 140

Gly Glu Val Gly Ala Pro Gly Met Gln Gly Ser Ala Gly Ala Arg Gly
 145 150 155 160

Leu Ala Gly Pro Lys Gly Glu Arg Gly Val Pro Gly Glu Arg Gly Val
 165 170 175

Pro Gly Asn Ala Gly Ala Ala Gly Ser Ala Gly Ala Met Gly Pro Gln
 180 185 190

Gly Ser Pro Gly Ala Arg Gly Pro Pro Gly Leu Lys Gly Asp Lys Gly
 195 200 205

Ile Pro Gly Asp Lys Gly Ala Lys Gly Glu Ser Gly Leu Pro Asp Val
 210 215 220

Ala Ser Leu Arg Gln Gln Val Glu Ala Leu Gln Gly Gln Val Gln His
 225 230 235 240

Leu Gln Ala Ala Phe Ser Gln Tyr Lys Lys Val Glu Leu Phe Pro Asn
 245 250 255

Gly Gln Ser Val Gly Glu Lys Ile Phe Lys Thr Ala Gly Phe Val Lys
 260 265 270

Pro Phe Thr Glu Ala Gln Leu Leu Cys Thr Gln Ala Gly Gly Gln Leu
 275 280 285

Ala Ser Pro Arg Ser Ala Ala Glu Asn Ala Ala Leu Gln Gln Leu Val
 290 295 300

Val Ala Lys Asn Glu Ala Ala Phe Leu Ser Met Thr Asp Ser Lys Thr
 305 310 315 320

Glu Gly Lys Phe Thr Tyr Pro Thr Gly Glu Ser Leu Val Tyr Ser Asn
 325 330 335

Trp Ala Pro Gly Glu Pro Asn Asp Asp Gly Gly Ser Glu Asp Cys Val
 340 345 350

Glu Ile Phe Thr Asn Gly Lys Trp Asn Asp Arg Ala Cys Gly Glu Lys
 355 360 365

Arg Leu Val Val Cys Glu Phe
 370 375